

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10|577,775A  
Source: IFWO  
Date Processed by STIC: 3/15/07

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 03/15/2007

PATENT APPLICATION: US/10/577,775A

TIME: 10:18:27

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03152007\J577775A.raw

```

3 <110> APPLICANT: KIM, TAE-YOON
4     BIO CLUE & SOLUTION CO., LT
6 <120> TITLE OF INVENTION: EC SOD and Cell transducing EC SOD and use thereof
8 <130> FILE REFERENCE: 1012679-000121
10 <140> CURRENT APPLICATION NUMBER: US 10/577,775A
12 <141> CURRENT FILING DATE: 2006-04-28
14 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/002757
15 <151> PRIOR FILING DATE: 2004-10-29
17 <150> PRIOR APPLICATION NUMBER: KR10-2003-0076629
18 <151> PRIOR FILING DATE: 2003-10-31
20 <160> NUMBER OF SEQ ID NOS: 33
22 <170> SOFTWARE: KopatentIn 1.71
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 18
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: primer
33 <400> SEQUENCE: 1
34 atgttgccct tcttgctc                                     18
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 18
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: primer
46 <400> SEQUENCE: 2
47 ttaagtgggc ttgcactc                                     18
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 33
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: primer
59 <400> SEQUENCE: 3
60 agtctcgaga tggtggcctt cttgttctac ggc                 33
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 28
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: primer
72 <400> SEQUENCE: 4

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73 gatcctcgag tggctttgca ctgctct      28
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 27
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: primer
85 <400> SEQUENCE: 5
86 atctctagaa tgctggcgct actgtgt      27
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 34
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: primer
98 <400> SEQUENCE: 6
99 atcgaatcct caggcggcct tgcactcgct ctct      34
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 30
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: primer
111 <400> SEQUENCE: 7
112 gatcctcgag tggacgggag aggactcggc      30
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 31
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: primer
124 <400> SEQUENCE: 8
125 gatcctcgag tcaggcggcc ttgcactcgc t      31
128 <210> SEQ ID NO: 9
129 <211> LENGTH: 30
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: primer
137 <400> SEQUENCE: 9
138 gatcctcgag tggacgggag aggactcggc      30
141 <210> SEQ ID NO: 10
142 <211> LENGTH: 31
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: primer
150 <400> SEQUENCE: 10
151 aatgctcgag tcactctgag tgctcccgcg c      31

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154 <210> SEQ ID NO: 11
155 <211> LENGTH: 240
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <220> FEATURE:
160 <221> NAME/KEY: PEPTIDE
161 <222> LOCATION: (1)..(240)
162 <223> OTHER INFORMATION: Human EC SOD
165 <400> SEQUENCE: 11
166 Met Leu Ala Leu Leu Cys Ser Cys Leu Leu Leu Ala Ala Gly Ala Ser
167   1           5           10           15
169 Asp Ala Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser Asp Ser Ala
170           20           25           30
172 Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile Trp Gln Glu
173           35           40           45
175 Val Met Gln Arg Arg Asp Asp Gly Thr Leu His Ala Ala Cys Gln
176           50           55           60
178 Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg Val Thr Gly
179           65           70           75           80
181 Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu Asp Ala Phe
182           85           90           95
184 Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser Ser Arg Ala
185           100          105          110
187 Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys Glu Ser Thr
188           115          120          125
190 Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln His Pro Gly
191           130          135          140
193 Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp Arg Tyr Arg
194 145          150          155          160
196 Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile Val Gly Arg
197           165          170          175
199 Ala Val Val Val His Ala Gly Glu Asp Leu Gly Arg Gly Gly Asn
200           180          185          190
202 Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu Ala Cys Cys
203           195          200          205
205 Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln Ala Arg Glu
206           210          215          220
208 His Ser Glu Arg Lys Lys Arg Arg Arg Glu Ser Glu Cys Lys Ala Ala
209 225          230          235          240
212 <210> SEQ ID NO: 12
213 <211> LENGTH: 231
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: TAT-EC SOD fusion protein
221 <400> SEQUENCE: 12
222 Arg Lys Lys Arg Arg Gln Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
223   1           5           10           15
225 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys

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```

226          20          25          30
228 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
229          35          40          45
231 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
232          50          55          60
234 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
235          65          70          75          80
237 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
238          85          90          95
240 Pro Asn Ser Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
241          100         105         110
243 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val
244          115         120         125
246 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
247          130         135         140
249 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly
250 145          150          155          160
252 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
253          165          170          175
255 Asp Leu Gly Arg Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
256          180          185          190
258 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
259          195          200          205
261 Trp Glu Arg Gln Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Arg
262          210          215          220
264 Glu Ser Glu Cys Lys Ala Ala
265 225          230
268 <210> SEQ ID NO: 13
269 <211> LENGTH: 218
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: TAT-delta HD/EC SOD fusion protein
277 <400> SEQUENCE: 13
278 Arg Lys Lys Arg Arg Gln Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
279 1          5          10          15
281 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys
282          20          25          30
284 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
285          35          40          45
287 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
288          50          55          60
290 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
291 65          70          75          80
293 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
294          85          90          95
296 Pro Asn Ser Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
297          100         105         110
299 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val

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300          115          120          125
302 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
303          130          135          140
305 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly
306 145          150          155          160
308 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
309          165          170          175
311 Asp Leu Gly Arg Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
312          180          185          190
314 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
315          195          200          205
317 Trp Glu Arg Gln Ala Arg Glu His Ser Glu
318          210          215
321 <210> SEQ ID NO: 14
322 <211> LENGTH: 231
323 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: R9-EC SOD fusion protein
330 <400> SEQUENCE: 14
331 Arg Arg Arg Arg Arg Arg Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
332 1          5          10          15
334 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys
335          20          25          30
337 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
338          35          40          45
340 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
341          50          55          60
343 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
344 65          70          75          80
346 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
347          85          90          95
349 Pro Asn Ser Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
350          100          105          110
352 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val
353          115          120          125
355 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
356          130          135          140
358 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly
359 145          150          155          160
361 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
362          165          170          175
364 Asp Leu Gly Arg Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
365          180          185          190
367 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
368          195          200          205
370 Trp Glu Arg Gln Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Arg
371          210          215          220
373 Glu Ser Glu Cys Lys Ala Ala

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**VERIFICATION SUMMARY**

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